

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/572,696
Source: IFWP
Date Processed by STIC: 03/29/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 03/29/2006

PATENT APPLICATION: US/10/572,696

TIME: 09:47:07

Input Set : A:\42-000400us sequence final.ST25.txt

Output Set: N:\CRF4\03292006\J572696.raw

3 <110> APPLICANT: Garvan Institute of Medical Research
 5 <120> TITLE OF INVENTION: Method of modulating bone growth, remodeling and adiposity
 7 <130> FILE REFERENCE: 42-000400US
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/572,696
 C--> 9 <141> CURRENT FILING DATE: 2006-03-20
 9 <160> NUMBER OF SEQ ID NOS: 20
 11 <170> SOFTWARE: PatentIn version 3.3
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1180
 15 <212> TYPE: DNA
 16 <213> ORGANISM: human neuropeptide Y1 receptor
 19 <220> FEATURE:
 20 <221> NAME/KEY: CDS
 21 <222> LOCATION: (7)..(1161)
 23 <400> SEQUENCE: 1
 24 aagctt atg aat tca aca tta ttt tcc cag gtt gaa aat cat tca gtc 48
 25 Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val
 26 1 5 10
 28 cac tct aat ttc tca gag aag aat gcc cag ctt ctg gct ttt gaa aat 96
 29 His Ser Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn
 30 15 20 25 30
 32 gat gat tgt cat ctg ccc ttg gcc atg ata ttt acc tta gct ctt gct 144
 33 Asp Asp Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala
 34 35 40 45
 36 tat gga gct gtg atc att ctt ggt gtc tct gga aac ctg gcc ttg atc 192
 37 Tyr Gly Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile
 38 50 55 60
 40 ata atc atc ttg aaa caa aag gag atg aga aat gtt acc aac atc ctg 240
 41 Ile Ile Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu
 42 65 70 75
 44 att gtg aac ctt tcc ttc tca gac ttg ctt gtt gcc atc atg tgt ctc 288
 45 Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu
 46 80 85 90
 48 ccc ttt aca ttt gtc tac aca tta atg gac cac tgg gtc ttt ggt gag 336
 49 Pro Phe Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu
 50 95 100 105 110
 52 gcg atg tgt aag ttg aat cct ttt gtg caa tgt gtt tca atc act gtg 384
 53 Ala Met Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val
 54 115 120 125
 56 tcc att ttc tct ctg gtt ctc att gct gtg gaa cga cat cag ctg ata 432
 57 Ser Ile Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile
 58 130 135 140
 60 atc aac cct cga ggg tgg aga cca aat aat aga cat gct tat gta ggt 480

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61 Ile Asn Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly
62      145      150      155
64 att gct gtg att tgg gtc ctt gct gtg gct tct tct ttg cct ttc ctg      528
65 Ile Ala Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu
66      160      165      170
68 atc tac caa gta atg act gat gag ccg ttc caa aat gta aca ctt gat      576
69 Ile Tyr Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp
70 175      180      185      190
72 gcg tac aaa gac aaa tac gtg tgc ttt gat caa ttt cca tcg gac tct      624
73 Ala Tyr Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser
74      195      200      205
76 cat agg ttg tct tat acc act ctc ctc ttg gtg ctg cag tat ttt ggt      672
77 His Arg Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly
78      210      215      220
80 cca ctt tgt ttt ata ttt att tgc tac ttc aag ata tat ata cgc cta      720
81 Pro Leu Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu
82      225      230      235
84 aaa agg aga aac aac atg atg gac aag atg aga gac aat aag tac agg      768
85 Lys Arg Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg
86      240      245      250
88 tcc agt gaa acc aaa aga atc aat atc atg ctg ctc tcc att gtg gta      816
89 Ser Ser Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val
90 255      260      265      270
92 gca ttt gca gtc tgc tgg ctc cct ctt acc atc ttt aac act gtg ttt      864
93 Ala Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe
94      275      280      285
96 gat tgg aat cat cag atc att gct acc tgc aac cac aat ctg tta ttc      912
97 Asp Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe
98      290      295      300
100 ctg ctc tgc cac ctc aca gca atg ata tcc act tgt gtc aac ccc ata      960
101 Leu Leu Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile
102      305      310      315
104 ttt tat ggg ttc ctg aac aaa aac ttc cag aga gac ttg cag ttc ttc      1008
105 Phe Tyr Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe
106      320      325      330
108 ttc aac ttt tgt gat ttc cgg tct cgg gat gat gat tat gaa aca ata      1056
109 Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile
110 335      340      345      350
112 gcc atg tcc acg atg cac aca gat gtt tcc aaa act tct ttg aag caa      1104
113 Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln
114      355      360      365
116 gca agc cca gtc gca ttt aaa aaa atc aac aac aat gat gat aat gaa      1152
117 Ala Ser Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu
118      370      375      380
120 aaa atc tga aactacttat agctctaga      1180
121 Lys Ile
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 384
127 <212> TYPE: PRT

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128 <213> ORGANISM: human neuropeptide Y1 receptor
130 <400> SEQUENCE: 2
132 Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val His Ser
133 1 5 10 15
136 Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn Asp Asp
137 20 25 30
140 Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala Tyr Gly
141 35 40 45
144 Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile
145 50 55 60
148 Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val
149 65 70 75 80
152 Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu Pro Phe
153 85 90 95
156 Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Ala Met
157 100 105 110
160 Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile
161 115 120 125
164 Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn
165 130 135 140
168 Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly Ile Ala
169 145 150 155 160
172 Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr
173 165 170 175
176 Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr
177 180 185 190
180 Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg
181 195 200 205
184 Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu
185 210 215 220
188 Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg
189 225 230 235 240
192 Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser
193 245 250 255
196 Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe
197 260 265 270
200 Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp
201 275 280 285
204 Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu
205 290 295 300
208 Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr
209 305 310 315 320
212 Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn
213 325 330 335
216 Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met
217 340 345 350
220 Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser
221 355 360 365
224 Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu Lys Ile

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225      370      375      380
228 <210> SEQ ID NO: 3
229 <211> LENGTH: 3747
230 <212> TYPE: DNA
231 <213> ORGANISM: human neuro peptide Y2 receptor
234 <220> FEATURE:
235 <221> NAME/KEY: CDS
236 <222> LOCATION: (496)..(1638)
238 <400> SEQUENCE: 3
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241 ctccagtgccc ctcccctgca ggaccatcgc ccgcagcctc tgcacctgtt ttcttggtgtt      120
243 taagggtggg gtttgcccc ctccccacgc tcccatctct gatcctcca ccttcacccg      180
245 cccaccccg cagtgagtg ggtgcccagg cgcgcttggc ctgagaggtc ggcagcagac      240
247 ccggcagcgc caaccgccc gccgctctga ctgctccggc tgcccgcccg cgcggcgcg      300
249 gctgtcctgg accctaggag gggacggaac cggacttgcc tttgggcacc ttccagggcc      360
251 ctctccaggt cggctggcta atcatcggac agacggactg cacacatctt gtttccgcgt      420
253 ctccgcaaaa acgcgaggtc caggtcagtt gtagactctt gtgctggttg caggccaagt      480
255 ggacctgtac tgaaa atg ggt cca ata ggt gca gag gct gat gag aac cag      531
256      Met Gly Pro Ile Gly Ala Glu Ala Asp Glu Asn Gln
257      1      5      10
259 aca gtg gaa gaa atg aag gtg gaa caa tac ggg cca caa aca act cct      579
260 Thr Val Glu Glu Met Lys Val Glu Gln Tyr Gly Pro Gln Thr Thr Pro
261      15      20      25
263 aga ggt gaa ctg gtc cct gac cct gag cca gag ctt ata gat agt acc      627
264 Arg Gly Glu Leu Val Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr
265      30      35      40
267 aag ctg att gag gta caa gtt gtt ctc ata ttg gcc tac tgc tcc atc      675
268 Lys Leu Ile Glu Val Gln Val Val Leu Ile Leu Ala Tyr Cys Ser Ile
269 45      50      55      60
271 atc ttg ctt ggg gta att ggc aac tcc ttg gtg atc cat gtg gtg atc      723
272 Ile Leu Leu Gly Val Ile Gly Asn Ser Leu Val Ile His Val Val Ile
273      65      70      75
275 aaa ttc aag agc atg cgc aca gta acc aac ttt ttc att gcc aat ctg      771
276 Lys Phe Lys Ser Met Arg Thr Val Thr Asn Phe Phe Ile Ala Asn Leu
277      80      85      90
279 gct gtg gca gat ctt ttg gtg aac act ctg tgt cta ccg ttc act ctt      819
280 Ala Val Ala Asp Leu Leu Val Asn Thr Leu Cys Leu Pro Phe Thr Leu
281      95      100      105
283 acc tat acc tta atg ggg gag tgg aaa atg ggt cct gtc ctg tgc cac      867
284 Thr Tyr Thr Leu Met Gly Glu Trp Lys Met Gly Pro Val Leu Cys His
285      110      115      120
287 ctg gtg ccc tat gcc cag ggc ctg gca gta caa gta tcc aca atc acc      915
288 Leu Val Pro Tyr Ala Gln Gly Leu Ala Val Gln Val Ser Thr Ile Thr
289 125      130      135      140
291 ttg aca gta att gcc ctg gac cgg cac agg tgc atc gtc tac cac cta      963
292 Leu Thr Val Ile Ala Leu Asp Arg His Arg Cys Ile Val Tyr His Leu
293      145      150      155
295 gag agc aag atc tcc aag cga atc agc ttc ctg att att ggc ttg gcc      1011
296 Glu Ser Lys Ile Ser Lys Arg Ile Ser Phe Leu Ile Ile Gly Leu Ala

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297	160	165	170	
299	tgg ggc atc agt gcc ctg ctg gca agt ccc ctg gcc atc ttc cgg gag	1059		
300	Trp Gly Ile Ser Ala Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu			
301	175 180 185			
303	tat tgc ctg att gag atc att ccg gac ttt gag att gtg gcc tgt act	1107		
304	Tyr Ser Leu Ile Glu Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr			
305	190 195 200			
307	gaa aag tgg cct ggc gag gag aag agc atc tat ggc act gtc tat agt	1155		
308	Glu Lys Trp Pro Gly Glu Glu Lys Ser Ile Tyr Gly Thr Val Tyr Ser			
309	205 210 215 220			
311	ctt tct tcc ttg ttg atc ttg tat gtt ttg cct ctg ggc att ata tca	1203		
312	Leu Ser Ser Leu Leu Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser			
313	225 230 235			
315	ttt tcc tac act cgc att tgg agt aaa ttg aag aac cat gtc agt cct	1251		
316	Phe Ser Tyr Thr Arg Ile Trp Ser Lys Leu Lys Asn His Val Ser Pro			
317	240 245 250			
319	gga gct gca aat gac cac tac cat cag cga agg caa aaa acc acc aaa	1299		
320	Gly Ala Ala Asn Asp His Tyr His Gln Arg Arg Gln Lys Thr Thr Lys			
321	255 260 265			
323	atg ctg gtg tgt gtg gtg gtg gtg ttt gcg gtc agc tgg ctg cct ctc	1347		
324	Met Leu Val Cys Val Val Val Val Phe Ala Val Ser Trp Leu Pro Leu			
325	270 275 280			
327	cat gcc ttc cag ctt gcc gtt gac att gac agc cag gtc ctg gac ctg	1395		
328	His Ala Phe Gln Leu Ala Val Asp Ile Asp Ser Gln Val Leu Asp Leu			
329	285 290 295 300			
331	aag gag tac aaa ctc atc ttc aca gtg ttc cac att atc gcc atg tgc	1443		
332	Lys Glu Tyr Lys Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys			
333	305 310 315			
335	tcc act ttt gcc aat ccc ctt ctc tat ggc tgg atg aac agc aac tac	1491		
336	Ser Thr Phe Ala Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr			
337	320 325 330			
339	aga aag gct ttc ctc tgc gcc ttc cgc tgt gag cag cgg ttg gat gcc	1539		
340	Arg Lys Ala Phe Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala			
341	335 340 345			
343	att cac tct gag gtg tcc gtg aca ttc aag gct aaa aag aac ctg gag	1587		
344	Ile His Ser Glu Val Ser Val Thr Phe Lys Ala Lys Lys Asn Leu Glu			
345	350 355 360			
347	gtc aga aag aac agt ggc ccc aat gac tct ttc aca gag gct acc aat	1635		
348	Val Arg Lys Asn Ser Gly Pro Asn Asp Ser Phe Thr Glu Ala Thr Asn			
349	365 370 375 380			
351	gtc taaggaagct gtggtgtgaa aatgtatgga tgaattctga ccagagctat	1688		
352	Val			
355	gaatctggtt gatggcggct cacaagtga aactgatttc ccattttaaa gaagaagtgg	1748		
357	atctaaatgg aagcatctgc tgtttaattc ctggaaaact ggctgggcag agcctgtgtg	1808		
359	aaaatactgg aattcaaaga taaggcaaca aaatggttta cttaacagtt ggttggttag	1868		
361	taggttgcatt tatgagtaaa agcagagaga agtacttttg attattttcc tggagtgaag	1928		
363	aaaacttgaa caagaaattg gtattatcaa agcattgctg agagacggtg ggaaaataag	1988		
365	ttgactttca aatcacgtta ggacctggat tgaggaggtg tgcagttcgc tgctccctgc	2048		
367	ttggcttatg aaaacaccac tgaacagaaa tttctccagg gagccacagg ctctccttca	2108		

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/572,696

DATE: 03/29/2006

TIME: 09:47:08

Input Set : A:\42-000400us sequence final.ST25.txt

Output Set: N:\CRF4\03292006\J572696.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date